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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Wed Jun 06 10:07:03 EDT 2007

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Application No: 10588555 Version No: 1.1

Input Set:**Output Set:**

Started: 2007-06-06 10:06:46.807
Finished: 2007-06-06 10:06:50.515
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 708 ms
Total Warnings: 2
Total Errors: 975
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 323	Invalid/missing amino acid numbering in SEQID (1) POS (328)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (5)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (10)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (15)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (20)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (25)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (30)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (35)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (40)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (45)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (50)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (55)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (60)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (65)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (70)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (75)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (80)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (85)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (90)

Input Set:

Output Set:

Started: 2007-06-06 10:06:46.807
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Total Warnings: 2
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Actual SeqID Count: 18

Error code	Error Description
E 323	Invalid/missing amino acid numbering SEQID (2)at Protein (94) This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (9)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (15)
E 341	'Xaa' position not defined SEQID (16) POS (96)
E 341	'Xaa' position not defined SEQID (16) POS (226)
E 341	'Xaa' position not defined SEQID (16) POS (233)
E 341	'Xaa' position not defined SEQID (16) POS (268)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)

SEQUENCE LISTING

<110> Svendsen, Allan
Minning, Stefan

<120> Protease Variants

<130> 10517.204-US

<140> 10588555

<141> 2007-06-01

<160> 18

<170> PatentIn version 3.3

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<212> DNA

<213> Bacillus licheniformis

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ggt att tct att tat tct tta ggt atg cac ccg gcc caa gcc gcg cca 96
Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
-75 -70 -65

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Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
-60 -55 -50

tcg gtt act tat gac cca cac att aag agc gat caa tac ggc ttg tat 192
Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
-45 -40 -35

tca aaa gcg ttt aca ggc acc ggc aaa gtg aat gaa aca aag gaa aaa 240
Ser Lys Ala Phe Thr Gly Thr Lys Val Asn Glu Thr Lys Glu Lys

-30	-25	-20	-15	
gct gaa aaa aag tca ccc gcc aaa gct cct tac agc att aaa tcg gtg Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val				288
-10	-5	-1 1		
att ggt tct gat gat cggtt aca agg gtc acc aac aca acc gca tat ccg Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro	5	10	15	336
tac aga gct atc gtt cat att tca agc agc atc ggt tca tgc acc gga Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly	20	25	30	384
tgg atg atc ggt ccg aaa acc gtc gca aca gcc gga cac tgc atc tat Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr	35	40	45	432
35			50	
gac aca tca agc ggt tca ttt gcc ggt aca gcc act gtt tcg ccg gga Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly	55	60	65	480
cggtt aac ggg aca agc tat cct tac ggc tca gtt aaa tcg acg cgc tac Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr	70	75	80	528
Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly	85	90	95	576
ttt att ccg tca gga tgg aga agc gga aac acc aat tac gat tac gga Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly	100	105	110	624
tac tcg tac act act tca tca ctt gtt ggg aca act gtt acc atc agc Tyr Ser Tyr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser	115	120	125	672
115			130	
ggc tac cca ggc gat aaa aca gca ggc aca caa tgg cag cat tca gga Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly	135	140	145	720
ccg att gcc atc tcc gaa acg tat aaa ttg cag tac gca atg gac acg Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr	150	155	160	768
150				
tac gga gga caa agc ggt tca ccg gta ttc gaa caa agc agc tcc aga Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg	165	170	175	816
165				
acg aac tgt agc ggt ccg tgc tcg ctt gcc gta cac aca aat gga gta Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val	180	185	190	864
180				
tac ggc ggc tcc tcg tac aac aga ggc acc ccg att aca aaa gag gtg Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val	195	200	205	912
195			210	

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<212> PRT
<213> Bacillus licheniformis

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Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
-75 -70 -65

Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
-60 -55 -50

Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
-45 -40 -35

Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
-30 -25 -20 -15

Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
-10 -5 -1 1

Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
5 10 15

Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
20 25 30

Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
35 40 45 50

Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
55 60 65

Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
70 75 80

Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
85 90 95

Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
100 105 110

Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
115 120 125 130

Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
135 140 145

Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
150 155 160

Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
165 170 175

Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
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215 220

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-120	-115	-110		
agt	ggg att cta tcc cca	gta aac gca act caa gct gag act ctt act		93
Ser	Gly Ile Leu Ser Pro	Val Asn Ala Thr Gln Ala Glu Thr Leu Thr		
-105	-100	-95	-90	
aaa tta aat aaa ata agt cag aag cag gaa cca tca tat aaa cta gat				141
Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp				
-85	-80	-75		
gaa gaa atg gat tat gtt cta att gat ttg gaa aca caa tct gaa tcg				189
Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser				
-70	-65	-60		
att att tcg ata gga gat aat acc gat ttg gga gat caa tcg ttt act				237
Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr				
-55	-50	-45		
tct tta ggg aag gtg gga cat gga gaa ctt gag aaa att aac tta gaa				285
Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu				
-40	-35	-30		
gaa ttt cgt aat cct aat tta aca gta gta gac ccg tta aca cgt aag				333
Glu Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys				
-25	-20	-15	-10	
cct att gaa caa aaa atc agc cct ttt gtt gtt ata ggc gat gat ggg				381
Pro Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly				
-5	-1	1	5	
aga aga caa gtt caa aat act tct ttc atg cca ttt cgt gca ctt act				429
Arg Arg Gln Val Gln Asn Thr Ser Phe Met Pro Phe Arg Ala Leu Thr				
10	15	20		
tat att gag ttt gga aac ctt aca agt aca tgg agt tgt tct gga ggt				477
Tyr Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly				
25	30	35		
gtg att gga aca gat tta gtt gtt act aat gca cat tgt gta gaa ggt				525
Val Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly				
40	45	50	55	
tct gtg tta gca ggt act gta gtt cct ggt atg aac aat agt cag tgg				573
Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp				
60	65	70		
gca tat ggg cat tat agg gtt act cag att atc tac cct gat caa tac				621
Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr				
75	80	85		
aga aat aac ggt gct tca gag ttt gat tat gct ata ctt aga gta gca				669
Arg Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala				
90	95	100		

cct gac tct gat gga cgt cat att gga aac aga gct gga att tta tct		717	
Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser			
105	110	115	
ttt aca gaa aca gga act gtt aac gaa aat act ttt cta aga acg tat		765	
Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr			
120	125	130	135
gga tac ccc ggt gat aaa ata tca gag aca aaa tta att tct ttg tgg		813	
Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp			
140	145	150	
gga atg gtt ggt cga tct gat gca ttt ttg cat cga gac cta ctg ttc		861	
Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe			
155	160	165	
tac aat atg gac acc tat ttt ggt caa tca ggt tct cct gta tta aac		909	
Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn			
170	175	180	
agc gta gat tca atg gtt gcg gtt cat aat gca ggg tat atc gtt ggt		957	
Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly			
185	190	195	
ggt aat agg gaa att aat ggt ggt cct aaa atc aga aga gat ttt aca		1005	
Gly Asn Arg Glu Ile Asn Gly Gly Pro Lys Ile Arg Arg Asp Phe Thr			
200	205	210	215
aac tta ttt aat caa atg aac		1026	
Asn Leu Phe Asn Gln Met Asn			
220			

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<213> Bacillus halmapalus AA513

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-105	-100	-95	-90

Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp		
-85	-80	-75

Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser		
-70	-65	-60

Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr
-55 -50 -45

Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu
-40 -35 -30

Glu Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys
-25 -20 -15 -10

Pro Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly
-5 -1 1 5

Arg Arg Gln Val Gln Asn Thr Ser Phe Met Pro Phe Arg Ala Leu Thr
10 15 20

Tyr Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly
25 30 35

Val Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly
40 45 50 55

Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp
60 65 70

Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr
75 80 85

Arg Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala
90 95 100

Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser
105 110 115

Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr
120 125 130 135

Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp
140 145 150

Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe
155 160 165

Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn

170

175

180

Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly
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Asn Leu Phe Asn Gln Met Asn
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<213> Bacillus licheniformis AC116

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Ile Ser Ile Phe Ser Ser Gly Ile Tyr Ser Ala Gln Ala Ala Ser Ser
-75 -70 -65

ccg cat acc cca gtc tcc agc gac cct tcg tac aag ccc ggc tcc acc 144
Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Gly Ser Thr
-60 -55 -50 -45

tat gat ccc aac ata aaa att gac aat aac ggc gca tat tcg aaa gcc 192
Tyr Asp Pro Asn Ile Lys Ile Asp Asn Asn Gly Ala Tyr Ser Lys Ala
-40 -35 -30

ttc gaa gga acc gga aca ccc ggc ggc tcc gtt cag gcc aaa ccg aaa 240
Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys
-25 -20 -15

aaa gaa tcg ccc gcc ggc ccg cct tac agc cct aaa tcg gta atc ggc 288
Lys Glu Ser Pro Ala Gly Pro Pro Tyr Ser Pro Lys Ser Val Ile Gly
-10 -5 -1 1

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